RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/070,277A_

Source: _/FW16_

Date Processed by STIC: _8/2/05_

ENTERED

IFW16

RAW SEQUENCE LISTING   DATE: 08/02/2005
PATENT APPLICATION: US/10/070,277A   TIME: 15:48:58

Input Set : **N:\KEISHA\10070277A.txt**
Output Set: **N:\CRF4\08022005\J070277A.raw**

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 3 <110> APPLICANT: Ehrhardt, Thomas
 4         Lerchl, Jens
 5         Nigel, Marc Stitt
 6         Zenner, Rita
 8 <120> TITLE OF INVENTION: Plant dihydroorotase
10 <130> FILE REFERENCE: 0050/50716
12 <140> CURRENT APPLICATION NUMBER: US 10/070,277A
13 <141> CURRENT FILING DATE: 2002-03-06
15 <150> PRIOR APPLICATION NUMBER: PCT/EP00/08581
16 <151> PRIOR FILING DATE: 2000-09-02
19 <160> NUMBER OF SEQ ID NOS: 9
22 <170> SOFTWARE: Microsoft Word 2003
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25 <211> LENGTH: 1271
26 <212> TYPE: DNA
27 <213> ORGANISM: Solanum tuberosum
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30 <221> NAME/KEY: CDS
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39 ctc cgt gat ggt gat gtt ctt aag gca gtt gtc tct cac agt gca cat   98
40 Leu Arg Asp Gly Asp Val Leu Lys Ala Val Val Ser His Ser Ala His
41 15                  20                  25                  30
43 cac ttt ggg agg gca ata gtc atg cca aat ttg aag cct cct atc act  146
44 His Phe Gly Arg Ala Ile Val Met Pro Asn Leu Lys Pro Pro Ile Thr
45                  35                  40                  45
47 acc act gct gct gct gta gca tac cgg gag gcg ata ttg aaa tct tta  194
48 Thr Thr Ala Ala Ala Val Ala Tyr Arg Glu Ala Ile Leu Lys Ser Leu
49                  50                  55                  60
51 cct gtt gat agt gat ttc aac cct ctt atg aca ctt tat ttg aca gat  242
52 Pro Val Asp Ser Asp Phe Asn Pro Leu Met Thr Leu Tyr Leu Thr Asp
53          65                  70                  75
55 aca acc agt cct atg gaa atc aaa cta gca aga gag agc cag gtc gta  290
56 Thr Thr Ser Pro Met Glu Ile Lys Leu Ala Arg Glu Ser Gln Val Val
57      80                  85                  90
59 ttt ggg gtg aag ttg tac cct gct ggt gcc acg aca aat tct caa gat  338
60 Phe Gly Val Lys Leu Tyr Pro Ala Gly Ala Thr Thr Asn Ser Gln Asp
61 95                  100                 105                 110
63 gga gtg act gat ctt ttc ggg aag tgt tta cca gtt cta caa gaa atg  386
64 Gly Val Thr Asp Leu Phe Gly Lys Cys Leu Pro Val Leu Gln Glu Met
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68 Val Glu His Asn Met Pro Leu Leu Val His Gly Glu Val Thr Asn Pro
69                    130                  135                  140
71 gag gtt gac atg ttt gat aga gaa aag gta ttc att gaa acg gtt cta   482
72 Glu Val Asp Met Phe Asp Arg Glu Lys Val Phe Ile Glu Thr Val Leu
73                    145                  150                  155
75 aga ccg ttg gtg cag aaa ttt cca caa ttg aag gtc gtg atg gag cat   530
76 Arg Pro Leu Val Gln Lys Phe Pro Gln Leu Lys Val Val Met Glu His
77        160                  165                  170
79 gtt acc acc att gat gct gtt aag ttt gtt gaa tct tgc act gaa gga   578
80 Val Thr Thr Ile Asp Ala Val Lys Phe Val Glu Ser Cys Thr Glu Gly
81 175                  180                  185                  190
83 ttt gtt gca gca act gtc acc cca caa cat ctt gtt ttg aac agg aat   626
84 Phe Val Ala Ala Thr Val Thr Pro Gln His Leu Val Leu Asn Arg Asn
85                    195                  200                  205
87 tct ctc ttc caa ggg ggc tta caa ccg cat aat tac tgc ctt cca gtc   674
88 Ser Leu Phe Gln Gly Gly Leu Gln Pro His Asn Tyr Cys Leu Pro Val
89                    210                  215                  220
91 ctc aaa aga gag atc cac agg gag gca ctt gtg tca gct gta aca agt   722
92 Leu Lys Arg Glu Ile His Arg Glu Ala Leu Val Ser Ala Val Thr Ser
93        225                  230                  235
95 gga agt aaa aga ttt ttt ctt ggg act gat agt gct cct cat gat aga   770
96 Gly Ser Lys Arg Phe Phe Leu Gly Thr Asp Ser Ala Pro His Asp Arg
97        240                  245                  250
99 cga aga aaa gag tgt tct tgt gga tgt gct ggt att tac aat gca cct   818
100 Arg Arg Lys Glu Cys Ser Cys Gly Cys Ala Gly Ile Tyr Asn Ala Pro
101 255                  260                  265                  270
103 gta gcc ttg tca gta tat gcg aag gtg ttt gaa aag gaa aat gca ctc   866
104 Val Ala Leu Ser Val Tyr Ala Lys Val Phe Glu Lys Glu Asn Ala Leu
105                    275                  280                  285
107 gac aag ctt gaa gca ttc act agc ttc aat gga cca gat ttt tat ggg   914
108 Asp Lys Leu Glu Ala Phe Thr Ser Phe Asn Gly Pro Asp Phe Tyr Gly
109                    290                  295                  300
111 ctt cct agg aac aac tca aag att aag ttg agt aag acg cca tgg aag   962
112 Leu Pro Arg Asn Asn Ser Lys Ile Lys Leu Ser Lys Thr Pro Trp Lys
113        305                  310                  315
115 gta ccc gaa tcc ttt tct tat gca tca gga gat att att ccc atg ttt   1010
116 Val Pro Glu Ser Phe Ser Tyr Ala Ser Gly Asp Ile Ile Pro Met Phe
117        320                  325                  330
119 gct ggt gaa atg ctc gac tgg ttg ccg gct cct ctc tgagaatcat   1056
120 Ala Gly Glu Met Leu Asp Trp Leu Pro Ala Pro Leu
121 335                  340                  345
123 ttgtcattct tgtactgtaa tattgtgatt caaccaaaga tatagactgt aggtgtatca 1116
125 tcttttcttt catgttgatt agatattatc acgatgataa tatcctttca gctaataaat 1176
127 tatggaaaca ataagctttg cacgctcacc aaagtgctcc tgtattctga agttcttaaa 1236
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134 <211> LENGTH: 346
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144              20                  25                  30
146 Gly Arg Ala Ile Val Met Pro Asn Leu Lys Pro Pro Ile Thr Thr Thr
147          35                  40                  45
149 Ala Ala Ala Val Ala Tyr Arg Glu Ala Ile Leu Lys Ser Leu Pro Val
150      50                  55                  60
152 Asp Ser Asp Phe Asn Pro Leu Met Thr Leu Tyr Leu Thr Asp Thr Thr
153 65                  70                  75                  80
155 Ser Pro Met Glu Ile Lys Leu Ala Arg Glu Ser Gln Val Val Phe Gly
156              85                  90                  95
158 Val Lys Leu Tyr Pro Ala Gly Ala Thr Thr Asn Ser Gln Asp Gly Val
159             100                 105                 110
161 Thr Asp Leu Phe Gly Lys Cys Leu Pro Val Leu Gln Glu Met Val Glu
162             115                 120                 125
164 His Asn Met Pro Leu Leu Val His Gly Glu Val Thr Asn Pro Glu Val
165         130                 135                 140
167 Asp Met Phe Asp Arg Glu Lys Val Phe Ile Glu Thr Val Leu Arg Pro
168 145                 150                 155                 160
170 Leu Val Gln Lys Phe Pro Gln Leu Lys Val Val Met Glu His Val Thr
171             165                 170                 175
173 Thr Ile Asp Ala Val Lys Phe Val Glu Ser Cys Thr Glu Gly Phe Val
174             180                 185                 190
176 Ala Ala Thr Val Thr Pro Gln His Leu Val Leu Asn Arg Asn Ser Leu
177             195                 200                 205
179 Phe Gln Gly Gly Leu Gln Pro His Asn Tyr Cys Leu Pro Val Leu Lys
180         210                 215                 220
182 Arg Glu Ile His Arg Glu Ala Leu Val Ser Ala Val Thr Ser Gly Ser
183 225                 230                 235                 240
185 Lys Arg Phe Phe Leu Gly Thr Asp Ser Ala Pro His Asp Arg Arg Arg
186             245                 250                 255
188 Lys Glu Cys Ser Cys Gly Cys Ala Gly Ile Tyr Asn Ala Pro Val Ala
189             260                 265                 270
191 Leu Ser Val Tyr Ala Lys Val Phe Glu Lys Glu Asn Ala Leu Asp Lys
192         275                 280                 285
194 Leu Glu Ala Phe Thr Ser Phe Asn Gly Pro Asp Phe Tyr Gly Leu Pro
195     290                 295                 300
197 Arg Asn Asn Ser Lys Ile Lys Leu Ser Lys Thr Pro Trp Lys Val Pro
198 305                 310                 315                 320
200 Glu Ser Phe Ser Tyr Ala Ser Gly Asp Ile Ile Pro Met Phe Ala Gly
201             325                 330                 335
203 Glu Met Leu Asp Trp Leu Pro Ala Pro Leu
204             340                 345
206 <210> SEQ ID NO: 3
207 <211> LENGTH: 1962
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209 <213> ORGANISM: Nicotiana tabacum
211 <220> FEATURE:
212 <221> NAME/KEY: CDS
213 <222> LOCATION: (305)..(1678)
215 <400> SEQUENCE: 3
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221 ttgtacactc ccattgtcgc ttccagtttt gtgccccaaa taaccttttc agtcatttgt 180
223 atcttagcat caacaacagt tgctgtctct cttttgttcg tccaatatac tgagcatttt 240
225 ttgagtagta atttgaaggg tttattcagt tgttaaatat ttgatttttg ttttgtttaa 300
227 gaaa atg aga caa agg gtt gga ttt gca ttg att aga gaa agc ttg tat 349
228      Met Arg Gln Arg Val Gly Phe Ala Leu Ile Arg Glu Ser Leu Tyr
229       1               5                  10                  15
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232 Arg Lys Leu Lys Pro Ser Ser Val Pro Arg His Tyr Cys Thr Ser Ser
233                  20                  25                  30
235 tca gct aat gtt cct cct att cct cca cct aag att cct cat tct tct 445
236 Ser Ala Asn Val Pro Pro Ile Pro Pro Pro Lys Ile Pro His Ser Ser
237              35                  40                  45
239 aaa aag gga agg ttg ttt aca gga gcc act att ggt cta cta ata gct 493
240 Lys Lys Gly Arg Leu Phe Thr Gly Ala Thr Ile Gly Leu Leu Ile Ala
241          50                  55                  60
243 ggg gga gct tat gca agt acg gtt gat gag gcc acc ttc tgt ggc tgg 541
244 Gly Gly Ala Tyr Ala Ser Thr Val Asp Glu Ala Thr Phe Cys Gly Trp
245          65                  70                  75
247 cta ttc tca gca aca aaa cta gta aat ccg ttc ttt gca ttt ctg gat 589
248 Leu Phe Ser Ala Thr Lys Leu Val Asn Pro Phe Phe Ala Phe Leu Asp
249  80                  85                  90                  95
251 cca gag gtt gct cac aaa ctg gcg gtc tct gct gca gcc cga gga tgg 637
252 Pro Glu Val Ala His Lys Leu Ala Val Ser Ala Ala Ala Arg Gly Trp
253                 100                 105                 110
255 gtt cca agg gag aag agg cca gat cct cct ata ttg ggc ctt gat gtg 685
256 Val Pro Arg Glu Lys Arg Pro Asp Pro Pro Ile Leu Gly Leu Asp Val
257             115                 120                 125
259 tgg gga aga agg ttc tca aat cct gtt ggt ctt gct gct ggt ttt gac 733
260 Trp Gly Arg Arg Phe Ser Asn Pro Val Gly Leu Ala Ala Gly Phe Asp
261         130                 135                 140
263 aag aat gct gag gct gtt gaa gga ttg ctt gga tta ggt ttt ggc ttt 781
264 Lys Asn Ala Glu Ala Val Glu Gly Leu Leu Gly Leu Gly Phe Gly Phe
265     145                 150                 155
267 gtt gag gtt ggc tca gta act ccc att cca cag gaa ggc aac cca aaa 829
268 Val Glu Val Gly Ser Val Thr Pro Ile Pro Gln Glu Gly Asn Pro Lys
269 160                 165                 170                 175
271 cca cgt ata ttt agg ttg cca aat gaa ggt gct ata ata aat agg tgt 877
272 Pro Arg Ile Phe Arg Leu Pro Asn Glu Gly Ala Ile Ile Asn Arg Cys
273                 180                 185                 190
275 ggc ttc aat agt gaa gga atc gtt gtg gtt gcc aaa cga ttg ggt gct 925
276 Gly Phe Asn Ser Glu Gly Ile Val Val Val Ala Lys Arg Leu Gly Ala
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280 Gln His Gly Lys Arg Lys Leu Glu Thr Ser Ser Thr Ser Ser Pro Ala
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283 gga gat gaa gtc aag cat gga ggg aaa gct ggt cct ggt att ctt ggt  1021
284 Gly Asp Glu Val Lys His Gly Gly Lys Ala Gly Pro Gly Ile Leu Gly
285         225               230               235
287 gtt aac ctt gga aag aat aaa aca agt gaa gac gct gca gca gat tat  1069
288 Val Asn Leu Gly Lys Asn Lys Thr Ser Glu Asp Ala Ala Ala Asp Tyr
289 240               245               250               255
291 gtg caa gga gtc cat aca tta tct cag tat gct gac tac ttg gta att  1117
292 Val Gln Gly Val His Thr Leu Ser Gln Tyr Ala Asp Tyr Leu Val Ile
293         260               265               270
295 aat atc tca tcc cca aat act cca gga cta cgc cag ctt cag gga aga  1165
296 Asn Ile Ser Ser Pro Asn Thr Pro Gly Leu Arg Gln Leu Gln Gly Arg
297         275               280               285
298 aag cag ttg aag gat ctt gtg aag aag gtt caa gca gct cgt gat gaa  1213
299 Lys Gln Leu Lys Asp Leu Val Lys Lys Val Gln Ala Ala Arg Asp Glu
300         290               295               300
302 atg cag tgg ggt gag gaa gga cct ccg cct tta ctt gtg aaa att gct  1261
303 Met Gln Trp Gly Glu Glu Gly Pro Pro Pro Leu Leu Val Lys Ile Ala
304         305               310               315
306 cca gat ttg tct aaa caa gat ctt gaa gat att gca gtg gtg gct gtt  1309
307 Pro Asp Leu Ser Lys Gln Asp Leu Glu Asp Ile Ala Val Val Ala Val
308 320               325               330               335
310 gct ctt cgt gtg gat gga ctg att ata tca aat act act gtc caa aga  1357
311 Ala Leu Arg Val Asp Gly Leu Ile Ile Ser Asn Thr Thr Val Gln Arg
312         340               345               350
314 cca gat tcc ata agt caa aac cct gtg gct caa gag gct ggt ggc ttg  1405
315 Pro Asp Ser Ile Ser Gln Asn Pro Val Ala Gln Glu Ala Gly Gly Leu
316         355               360               365
318 agt ggg aag cca ctc ttt gac atg tca aca aat ata ctg aag gag atg  1453
319 Ser Gly Lys Pro Leu Phe Asp Met Ser Thr Asn Ile Leu Lys Glu Met
320         370               375               380
322 tac gtt ctg act aag gga agg att cct ctg att ggc act ggg ggt att  1501
323 Tyr Val Leu Thr Lys Gly Arg Ile Pro Leu Ile Gly Thr Gly Gly Ile
324         385               390               395
326 agc agt ggc gag gat gct tac aag aaa att cga gct ggt gcc act ctt  1549
327 Ser Ser Gly Glu Asp Ala Tyr Lys Lys Ile Arg Ala Gly Ala Thr Leu
328 400               405               410               415
330 gtt cag ctt tat aca gca ttt gca tat gga ggc cct gca ctt atc ccc  1597
331 Val Gln Leu Tyr Thr Ala Phe Ala Tyr Gly Gly Pro Ala Leu Ile Pro
332         420               425               430
334 gat ata aag gat gaa ctt gct cgt tgc tta gaa aag gat ggt tat aag  1645
335 Asp Ile Lys Asp Glu Leu Ala Arg Cys Leu Glu Lys Asp Gly Tyr Lys
336         435               440               445
338 tca atc agt gag gct gtt gga gca gac tgc aga tagtagtagt tgatatacta 1698
339 Ser Ile Ser Glu Ala Val Gly Ala Asp Cys Arg
340         450               455
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VERIFICATION SUMMARY   DATE: 08/02/2005
PATENT APPLICATION: **US/10/070,277A** TIME: 15:48:59

Input Set : **N:\KEISHA\10070277A.txt**
Output Set: **N:\CRF4\08022005\J070277A.raw**